26. (New) A method according to claim 25, wherein the DNA sequence comprises an expression-enhancing quality.

27. (New) A method according to claim 26, wherein the transcription system comprises host cells.

28. (New) A method according to claim 25, wherein the cloned DNA fragments have a size of 5,000 base pairs.

29. (New) A method according to claim 25, wherein the distance between the DNA sequence involved in gene repressing chromatin and the reporter gene is fewer than 5,000 base pairs.

30. (New) A method according to claim 25, wherein the promoter may be active in the transcription system but wherein induction of gene-repressing chromatin in the vectors results in the repression of the transcription of the reporter gene.

31. (New) A method according to claim 25, wherein the selection in step 3) occurs by using a reporter gene which provides resistance to a growth inhibitor.

32. (New) A method according to claim 31, wherein the host cells are cultivated in the presence of the growth inhibitor.

33. (New) A method according to claim 32, wherein the growth inhibitor is present in a concentration sufficiently high to kill host cells in which the gene providing resistance to the growth inhibitor is not active.

34. (New) A method according to claim 33, wherein an antibiotic is used as the growth inhibitor and the reporter gene provides resistance to the antibiotic.

35. (New) A method according to claim 34, wherein the reporter gene codes for Green Fluorescent Protein.

36. (New) A method according to claim 35, wherein the reporter gene is luciferase.

37. (New) A method according to claim 36, wherein the fluorescent host cells are separated from non-fluorescent host cells by means of a Fluorescence-Activated Cell Sorter (FACS).

38. (New) A method according to claim 29, wherein the cloned DNA fragments have a size of substantially between 2,000-3,000 base pairs.

39. (New) A method according to claim 25, wherein the DNA sequence involved with the transcription induction of gene-repressing chromatin is a DNA sequence that is recognized by a heterochromatin-binding protein comprising HP1, which HP1-comprising complex is present in the transcription system and/or the host cell.

40. (New) A method according to claim 25, wherein the DNA sequence involved with the transcription induction of gene-repressing chromatin is a DNA sequence that is recognized by a complex comprising a Polycomb-group (Pc-G) protein, and the Polycomb-group protein-comprising complex is present in the transcription system and/or in the host cell.

41. (New) A method according to claim 25, wherein the DNA sequence involved with the transcription induction of gene-repressing chromatin is a DNA sequence that is recognized by a complex possessing a histone deacetylase activity, and the histone deacetylase activity-possessing complex is present in the transcription system and/or in the host cell.

42. (New) A method according to claim 25, wherein the DNA sequence involved in the transcription induction of gene-repressing chromatin is a DNA sequence that is recognized by a protein complex comprising MeCP2 (methyl-CpG-binding protein 2), and the MeCp2-comprising complex is present in the transcription system and/or in the host cell.

43. (New) A method according to claim 25, wherein the DNA sequence involved with the transcription inducing of gene-repressing chromatin is a DNA sequence that is selectively recognized by at least one DNA-binding protein and the organism also expresses a protein complex comprising i) a first part selectively binding the DNA sequence, and ii) a second part inducing the formation of chromatin in which the transcription is repressed.

44. (New) A method according to claim 43, wherein the protein complex comprises a fusion protein.

45. (New) A method according to claim 44, wherein first part is a part binding the DNA binding site of LexA-DNA or GAL4-DNA.

46. (New) A method according to claim 25, wherein the organism in step 1) is selected from the group comprising a plant and a vertebrate.

47. (New) A method according to claim 46, wherein the vertebrate is a mammal.

48. (New) A method according to claim 25, wherein the vector is an episomally replicating vector.

49. (New) A method according to claim 48, wherein the vector comprises a replication origin from the Epstein-Barr virus (EBV), OriP, and a nuclear antigen (EBNA1).

50. (New) A DNA sequence selected from i) a DNA sequence isolated from a plant or vertebrate, or derivatives thereof, and ii) a synthetic DNA sequence or one constructed by means of genetic engineering, which DNA sequence is a repression-inhibiting sequence which, by the method according to the present invention can be detected, selected and optionally cloned.

51. (New) A DNA sequence selected from i) a DNA sequence isolated from a plant or vertebrate, or derivatives thereof, and ii) a synthetic DNA sequence is detected, selected and optionally cloned by the method set forth in claim 25.

52. (New) A method of making a DNA construct comprising a gene that is to be expressed stably, wherein a stable expression-promoting DNA sequence is integrated in accordance with claim 51.

53. (New) A method according to claim 52, wherein the DNA sequence is integrated in fewer than 2,000 bp of the gene.

54. (New) A method according to claim 52, wherein the stable expression-modulating DNA sequence will be integrated both upstream and downstream from the gene.

55. (New) A method according to claim 54 wherein the DNA sequence comprises an expression enhancing DNA sequence.